```
GTCAATATGCTGTTCAAGTCATGGCAACTGGCAGCAGCCTCCGGGCTCCTGTCTGGAGTC    60
       MetLeuPheLysSerTrpGlnLeuAlaAlaAlaSerGlyLeuLeuSerGlyVa    18

CTCGGCATCCCGATGGACACCGGCAGCCACCCCATTGAGGCTGTTGATCCCGAAGTGAAG   120
lLeuGlyIleProMetAspThrGlySerHisProIleGluAlaValAspProGluValLy    38

ACTGAGGTCTTCGCTGACTCCCTCCTTGCTGCAGCAGGCGATGACGACTGGGAGTCACCT   180
sThrGluValPheAlaAspSerLeuLeuAlaAlaAlaGlyAspAspAspTrpGluSerPr    58

CCATACAACTTGCTTTACAGGAATGCCCTGCCAATTCCACCTGTCAAGCAGCCCAAGATG   240
oProTyrAsnLeuLeuTyrArgAsnAlaLeuProIleProProValLysGlnProLysMe    78

ATCATTACCAACCCTGTCACCGGCAAGGACATTTGGTACTATGAGATCGAGATCAAGCCA   300
tIleIleThrAsnProValThrGlyLysAspIleTrpTyrTyrGluIleGluIleLysPr    98

TTTCAGCAAAGGATTTACCCCACCTTGCGCCCTGCCACTCTCGTCGGCTACGATGGCATG   360
oPheGlnGlnArgIleTyrProThrLeuArgProAlaThrLeuValGlyTyrAspGlyMe   118

AGCCCTGGTCCTACTTTCAATGTTCCCAGAGGAACAGAGACTGTAGTTAGGTTCATCAAC   420
tSerProGlyProThrPheAsnValProArgGlyThrGluThrValValArgPheIleAs   138

AATGCCACCGTGGAGAACTCGGTCCATCTGCACGGCTCCCCATCGCGTGCCCCTTTCGAT   480
nAsnAlaThrValGluAsnSerValHisLeuHisGlySerProSerArgAlaProPheAs   158

GGTTGGGCTGAAGATGTGACCTTCCCTGGCGAGTACAAGGATTACTACTTTCCCAACTAC   540
pGlyTrpAlaGluAspValThrPheProGlyGluTyrLysAspTyrTyrPheProAsnTy   178

CAATCCGCCCGCCTTCTGTGGTACCATGACCACGCTTTCATGAAGACTGCTGAGAATGCC   600
rGlnSerAlaArgLeuLeuTrpTyrHisAspHisAlaPheMetLysThrAlaGluAsnAl   198

TACTTTGGTCAGGCTGGCGCCTACATTATCAACGACGAGGCTGAGGATGCTCTCGGTCTT   660
aTyrPheGlyGlnAlaGlyAlaTyrIleIleAsnAspGluAlaGluAspAlaLeuGlyLe   218

CCTAGTGGCTATGGCGAGTTCGATATCCCTCTGATCCTGACGGCCAAGTACTATAACGCC   720
uProSerGlyTyrGlyGluPheAspIleProLeuIleLeuThrAlaLysTyrTyrAsnAl   238

GATGGTACCCTGCGTTCGACCGAGGGTGAGGACCAGGACCTGTGGGGAGATGTCATCCAT   780
aAspGlyThrLeuArgSerThrGluGlyGluAspGlnAspLeuTrpGlyAspValIleHi   258

GTCAACGGACAGCCATGGCCTTTCCTTAACGTCCAGCCCCGCAAGTACCGTTTCCGATTC   840
sValAsnGlyGlnProTrpProPheLeuAsnValGlnProArgLysTyrArgPheArgPh   278

CTCAACGCTGCCGTGTCTCGTGCTTGGCTCCTCTACCTCGTCAGGACCAGCTCTCCCAAC   900
eLeuAsnAlaAlaValSerArgAlaTrpLeuLeuTyrLeuValArgThrSerSerProAs   298

GTCAGAATTCCTTTCCAAGTCATTGCCTCTGATGCTGGTCTCCTTCAAGCCCCCGTTCAG   960
nValArgIleProPheGlnValIleAlaSerAspAlaGlyLeuLeuGlnAlaProValGl   318

ACCTCTAACCTCTACCTTGCTGTTGCCGAGCGTTACGAGATCATTATTGACTTCACCAAC  1020
nThrSerAsnLeuTyrLeuAlaValAlaGluArgTyrGluIleIleIleAspPheThrAs   338

TTTGCTGGCCAGACTCTTGACCTGCGCAACGTTGCTGAGACCAACGATGTCGGCGACGAG  1080
nPheAlaGlyGlnThrLeuAspLeuArgAsnValAlaGluThrAsnAspValGlyAspGl   358

GATGAGTACGCTCGCACTCTCGAGGTGATGCGCTTCGTCGTCAGCTCTGGCACTGTTGAG  1140
uAspGluTyrAlaArgThrLeuGluValMetArgPheValValSerSerGlyThrValGl   378
```

FIG._1A

```
GACAACAGCCAGGTCCCCTCCACTCTCCGTGACGTTCCTTTCCCTCCTCACAAGGAAGGC    1200
uAspAsnSerGlnValProSerThrLeuArgAspValProPheProProHisLysGluGl    398

CCCGCCGACAAGCACTTCAAGTTTGAACGCAGCAACGGACACTACCTGATCAACGATGTT    1260
yProAlaAspLysHisPheLysPheGluArgSerAsnGlyHisTyrLeuIleAsnAspVa    418

GGCTTTGCCGATGTCAATGAGCGTGTCCTGGCCAAGCCCGAGCTCGGCACCGTTGAGGTC    1320
lGlyPheAlaAspValAsnGluArgValLeuAlaLysProGluLeuGlyThrValGluVa    438

TGGGAGCTCGAGAACTCCTCTGGAGGCTGGAGCCACCCCGTCCACATTCACCTTGTTGAC    1380
lTrpGluLeuGluAsnSerSerGlyGlyTrpSerHisProValHisIleHisLeuValAs    458

TTCAAGATCCTCAAGCGAACTGGTGGTCGTGGCCAGGTCATGCCCTACGAGTCTGCTGGT    1440
pPheLysIleLeuLysArgThrGlyGlyArgGlyGlnValMetProTyrGluSerAlaGl    478

CTTAAGGATGTCGTCTGGTTGGGCAGGGGTGAGACCCTGACCATCGAGGCCCACTACCAA    1500
yLeuLysAspValValTrpLeuGlyArgGlyGluThrLeuThrIleGluAlaHisTyrGl    498

CCCTGGACTGGAGCTTACATGTGGCACTGTCACAACCTCATTCACGAGGATAACGACATG    1560
nProTrpThrGlyAlaTyrMetTrpHisCysHisAsnLeuIleHisGluAspAsnAspMe    518

ATGGCTGTATTCAACGTCACCGCCATGGAGGAGAAGGGATATCTTCAGGAGGACTTCGAG    1620
tMetAlaValPheAsnValThrAlaMetGluGluLysGlyTyrLeuGlnGluAspPheGl    538

GACCCCATGAACCCCAAGTGGCGCGCCGTTCCTTACAACCGCAACGACTTCCATGCTCGC    1680
uAspProMetAsnProLysTrpArgAlaValProTyrAsnArgAsnAspPheHisAlaAr    558

GCTGGAAACTTCTCCGCCGAGTCCATCACTGCCCGAGTGCAGGAGCTGGCCGAGCAGGAG    1740
gAlaGlyAsnPheSerAlaGluSerIleThrAlaArgValGlnGluLeuAlaGluGlnGl    578

CCGTACAACCGCCTCGATGAGATCCTGGAGGATCTTGGAATCGAGGAGTAA             1791
uProTyrAsnArgLeuAspGluIleLeuGluAspLeuGlyIleGluGlu               594
```

FIG._1B

```
CTGGCTAGCC TCACTTGGTA GACAGCCCTG ACAGCCTCAC TGGCTGGGGG TCGAAAGGCC   60
AGTCAATATC TTGGTCACTG CTAATAGTTC CTTGCTACGC GCAAAAAGCT CCTTGCCGAA  120
GGGGCACAGA CTATCAAGTG AGACATATAG GATGCATGTC TTTCATAGCC ACAGTTAGGG  180
TGGTGACCTA CTCGAAGAGG CCCCGACTTG CATGCATACG ACATGTCGCT TCCATGCAAC  240
ATGTATGCGC ACATCGGCGA TCAGGCACCC TCTGCATGCA GAATAGAACC CCCCTGGTTT  300
CCTTTTGTTT CTTTTCCTTT CTCAACGACG CGTGAGCGTG GTTAACTTGA GCAAGGCCGA  360
GTGGTCTGTT CACGAGGTTA CCATCGAACT CTCTTCTTTC CCAATCATGA CCTGCCCCCC  420
GAGTTTAGCC CCCATCACGG CTGTGAAATC CACTTCGATA ATCCTAGCCT AGTGCTACTC  480
TTCAATAGTT GCTCCTGATG GGGCACTTTG GTCACATTGC CTTGGTTYCT CCTACCTCGT  540
TCTCTTCCGC ATCAAGCCTC TATGCCCGAC GACAACACCT CATTGGCCCG GACCACTTTG  600
AGCGCGCACG CACCTTCGCG CCGAAGGAGT TGATAACACC CTTCACCCTT GCCCAATGAT  660
GGAGTTTTGG TCTATTTGTC ATGATCACCT CACATTCACT AGATCACGGA TCCTGGAAGA  720
GGGTGTGGAA GCCAGACCAG CTTGTCCCTG TTCTTGCAGA CTCAGGTCAG CTCCTAGCGG  780
CTATCACAGC TCAGGATTAT CAAGTCCCGT AAAGTCCAGA CCCTTTTCAT TGTATGATGC  840
TGCCTAATTT GCGCTATCTC TATGCCGTAG CAGCCGTCTT GGCTACAACT GGCTGCCATG  900
GCTGAAGCAT CGTGAGATCT ATAAAGGTCT CCGAATCCTC GGTGAAGTCA GAATCGTCTC  960
TCCACACCAG TCAACAACAA GCTTCTTTCT CTTACAGCTT AGCCTGAGCA CATTCACAGA 1020
ACTCTTCCCT TCTTTTCGTC AATATGCTGT TCAAGTCATG GCAACTGGCA GCAGCCTCCG 1080
GGCTCCTGTC TGGAGTCCTC GGCATCCCGA TGGACACCGG CAGCCACCCC ATTGAGGCTG 1140
TTGATCCCGA AGTGAAGACT GAGGTCTTCG CTGACTCCCT CCTTGCTGCA GCAGGCGATG 1200
ACGACTGGGA GTCACCTCCA TACAACTTGC TTTACAGGTG AGACACCTGT CCCACCTGTT 1260
TTCCCTCGAT AACTAACTCT TATAGGAATG CCCTGCCAAT TCCACCTGTC AAGCAGCCCA 1320
AGATGTATGT CTTTGATTTT CTACGAAGCA ACTCGGCCCC GACTAATGTA TTCTAGGATC 1380
ATTACCAACC CTGTCACCGG CAAGGACATT TGGTACTATG AGATCGAGAT CAAGCCATTT 1440
CAGCAAAGGG TGAGTTTGCT CAGAAACCTT GTGGTAATTA ATCATTGTTA CTGACCCTTT 1500
CAGATTTACC CCACCTTGCG CCCTGCCACT CTCGTCGGCT ACGATGGCAT GAGCCCTGGT 1560
CCTACTTTCA ATGTTCCCAG AGGAACAGAG ACTGTAGTTA GGTTCATCAA CAATGCCACC 1620
GTGGAGAACT CGGTCCATCT GCACGGCTCC CCATCGCGTG CCCCTTTCGA TGGTTGGGCT 1680
GAAGATGTGA CCTTCCCTGG CGAGTACAAG GATTACTACT TTCCCAACTA CCAATCCGCC 1740
CGCCTTCTGT GGTACCATGA CCACGCTTTC ATGAAGGTAT GCTACGAGCC TTTATCTTTC 1800
TTGGCTACCT TTGGCTAACC AACTTCCTTT CGTAGACTGC TGAGAATGCC TACTTTGGTC 1860
AGGCTGGCGC CTACATTATC AACGACGAGG CTGAGGATGC TCTCGGTCTT CCTAGTGGCT 1920
ATGGCGAGTT CGATATCCCT CTGATCCTGA CGGCCAAGTA CTATAACGCC GATGGTACCC 1980
TGCGTTCGAC CGAGGGTGAG GACCAGGACC TGTGGGGAGA TGTCATCCAT GTCAACGGAC 2040
AGCCATGGCC TTTCCTTAAC GTCCAGCCCC GCAAGTACCG TTTCCGATTC CTCAACGCTG 2100
CCGTGTCTCG TGCTTGGCTC CTCTACCTCG TCAGGACCAG CTCTCCCAAC GTCAGAATTC 2160
CTTTCCAAGT CATTGCCTCT GATGCTGGTC TCCTTCAAGC CCCCGTTCAG ACCTCTAACC 2220
TCTACCTTGC TGTTGCCGAG CGTTACGAGA TCATTATTGG TATGCCCTCC CCTCTCACGA 2280
ATGAGTCAAG AACTCTAAGA CTAACACTTG TAGACTTCAC CAACTTTGCT GGCCAGACTC 2340
TTGACCTGCG CAACGTTGCT GAGACCAACG ATGTCGGCGA CGAGGATGAG TACGCTCGCA 2400
CTCTCGAGGT GATGCGCTTC GTCGTCAGCT CTGGCACTGT TGAGGACAAC AGCCAGGTCC 2460
CCTCCACTCT CCGTGACGTT CCTTTCCCTC CTCACAAGGA AGGCCCCGCC GACAAGCACT 2520
TCAAGTTTGA ACGCAGCAAC GGACACTACC TGATCAACGA TGTTGGCTTT GCCGATGTCA 2580
ATGAGCGTGT CCTGGCCAAG CCCGAGCTCG GCACCGTTGA GGTCTGGGAG CTCGAGAACT 2640
CCTCTGGAGG CTGGAGCCAC CCCGTCCACA TTCACCTTGT TGACTTCAAG ATCCTCAAGC 2700
GAACTGGTGG TCGTGGCCAG GTCATGCCCT ACGAGTCTGC TGGTCTTAAG GATGTCGTCT 2760
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ACATGTGGCA CTGTCACAAC CTCATTCACG AGGATAACGA CATGATGGCT GTATTCAACG 2880
TCACCGCCAT GGAGGAGAAG GGATATCTTC AGGAGGACTT CGAGGACCCC ATGAACCCCA 2940
AGTGGCGCGC CGTTCCTTAC AACCGCAACG ACTTCCATGC TCGCGCTGGA AACTTCTCCG 3000
CCGAGTCCAT CACTGCCCGA GTGCAGGAGC TGGCCGAGCA GGAGCCGTAC AACCGCCTCG 3060
ATGAGATCCT GGAGGATCTT GGAATCGAGG AGTAAACCCC GAGCCACAAG CTCTACAATC 3120
GTTTTGAGTC TTAAGACGAG GCTCTTGGTG CGTATTCTTT TCTTCCCTAC GGGGAACTCC 3180
GCTGTCCACT GCGATGTGAA GGACCATCAC AAAGCAACGT ATATATTGGA CTCACCACTG 3240
TCATTACCGC CCACTTGTAC CTATTCGATT CTTGTTCAAA CTTTTCTAGT GCGAGAGTGT 3300
CCATAGTCAA GAAACGCCCA TAGGGCTATC GTCTAAACTG AACTATTGTG TGGTCTGTGA 3360
CGTGGAGTAG ATGTCAATTG TGATGAGACA CAGTAAATAC GGTATATCTT TTCCTAGGAC 3420
TACAGGATCA GTTTCTCATG AGATTACATC CGTCTAATGT TTGTCCATGA GAGTCTAGCT 3480
AAGGTTGAGA ATGCATCAGA CGGAATCATT TGATGCTCTC AGCTCGTATT ACCGATGTAA 3540
GACAAGTTAG GTAAGTTGCT TGGTATCCGA AAATGACTCA GGCTCCCTCA TTAGGTTGCA 3600
TGTGAAAACC TTCAGCAACT CATGGGTGTT GGGACCAAAT CATCCATACC TGATTTTGAT 3660
AACTGACCTG GGTCAAT                                               3677
```
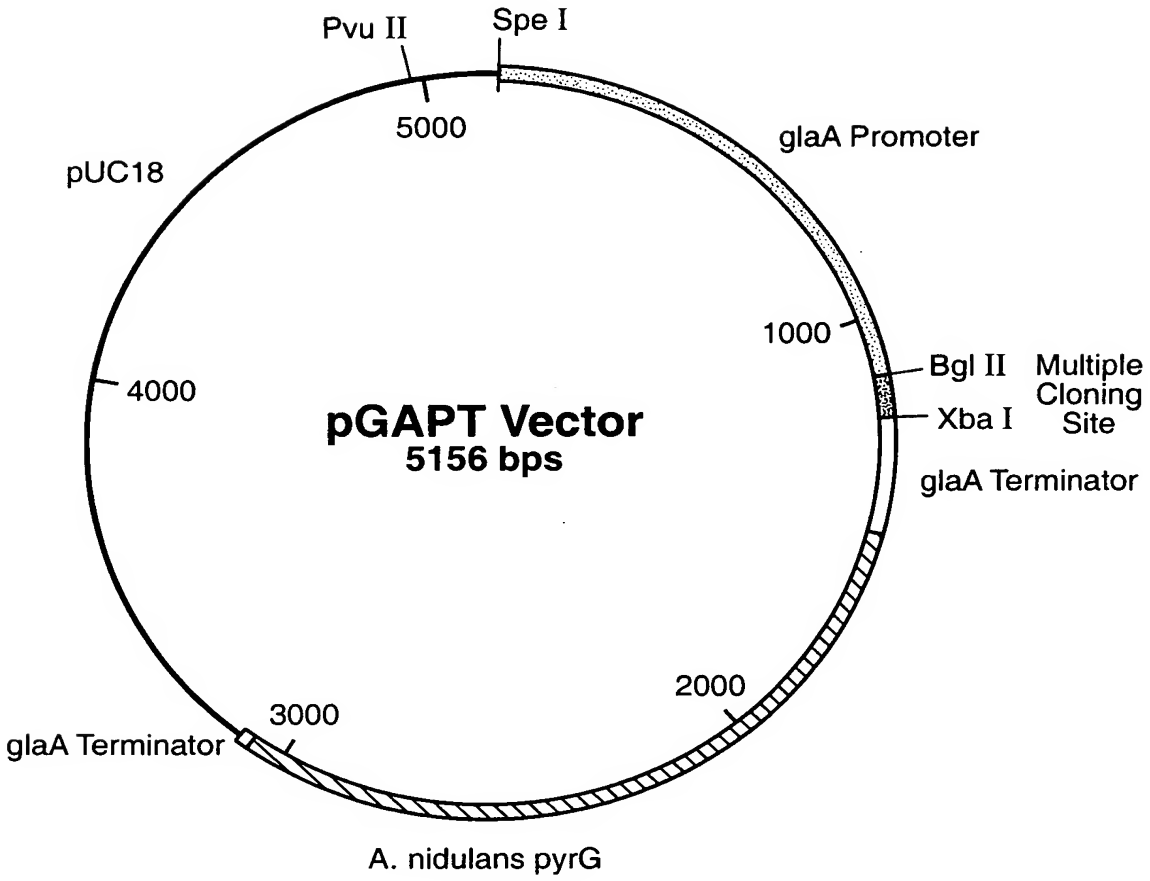

FIG._2

```
  1  ..........MFKHTLGAAALSLLFNSNAVQA.SPVPETSPATGHLFKRV   39
                     |         |    |  |   |      |
  1  MLFKSWQLAAASGLLSGVLGIPMDTGSHPIEAVDPEVKTEVFADSLLAAA   50

 40  AQISPQYPMFTV....PLPIPPVKQPRLTVTNPVNGQEIWYYEVEIKPFT   85
            |         |||||||||    |||| |  ||||| |||||
 51  GDDDWESPPYNLLYRNALPIPPVKQPKMIITNPVTGKDIWYYEIEIKPFQ  100

 86  HQVYPDLGSADLVGYDGMSPGPTFQVPRGVETVVRFINNAEAPNSVHLHG  135
        || |  | ||||||||||||| |||| ||||||||||   |||||||
101  QRIYPTLRPATLVGYDGMSPGPTFNVPRGTETVVRFINNATVENSVHLHG  150

136  SFSRAAFDGWAEDITEPGSFKDYYYPNRQSARTLWYHDHAMHITAENAYR  185
     | ||| ||||||| | ||  |||| || |||| |||||||   ||||||
151  SPSRAPFDGWAEDVTFPGEYKDYYFPNYQSARLLWYHDHAFMKTAENAYF  200

186  GQAGLYMLTDPAEDALNLPSGYGEFDIPMILTSKQYTANGNLVTTNGELN  235
     |||| |   | ||||| ||||||||||| ||| | | | | |  | ||
201  GQAGAYIINDEAEDALGLPSGYGEFDIPLILTAKYYNADGTLRSTEGEDQ  250

236  SFWGDVIHVNGQPWPFKNVEPRKYRFRFLDAAVSRSFGLYFADTDAIDTR  285
       |||||||||||||| || ||||||||| |||||   ||   |     |
251  DLWGDVIHVNGQPWPFLNVQPRKYRFRFLNAAVSRAWLLYLVRTSSPNVR  300

286  LPFKVIASDSGLLEHPADTSLLYISMAERYEVVFDFSDYAGKTIELRNLG  335
      || ||||| |||  |  || ||   |||||   ||   || |  |||
301  IPFQVIASDAGLLQAPVQTSNLYLAVAERYEIIIDFTNFAGQTLDLRNV.  349

336  GSIGGIGTDTDYDNTDKVMRFVVADDTTQPDTSVVPANLRDVPFPSPTTN  385
           |    |  |  ||||||   |   | | ||  |||||||
350  AETNDVGDEDEYARTLEVMRFVVSSGTVE.DNSQVPSTLRDVPFPPHKEG  398

386  .TPRQFRFGRTGPTWTINGVAFADVQNRLLANVPVGTVERWELINAGNGW  434
          | | |      || | ||||  | ||    |||| ||| |   ||
399  PADKHFKFERSNGHYLINDVGFADVNERVLAKPELGTVEVWELENSSGGW  448

435  THPIHIHLVDFKVISRTSGNNARTVMPYES.GLKDVVWLGRRETVVVEAH  483
      || ||||||||   || |     |||||| |||||||||| ||   |||
449  SHPVHIHLVDFKILKRTGGRG..QVMPYESAGLKDVVWLGRGETLTIEAH  496

484  YAPFPGVYMFHCHNLIHEDHDMMAAFNATVLPDYGYNATVFVDPMEELWQ  533
     | |  | || ||||||||| |||| || |     ||    | |||   |.
497  YQPWIGAYMWHCHNLIHEDNDMMAVFNVTAMEEKGYLQEDFEDPMNPKWR  546

534  ARPYELGEFQAQSGQFSVQAVTERIQTMAEYRPYAAADE.........   572
     | ||    | |  | ||    |   |  ||  ||   ||
547  AVPYNRNDFHARAGNFSAESITARVQELAEQEPYNRLDEILEDLGIEE   594
```

FIG._3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Bgl II
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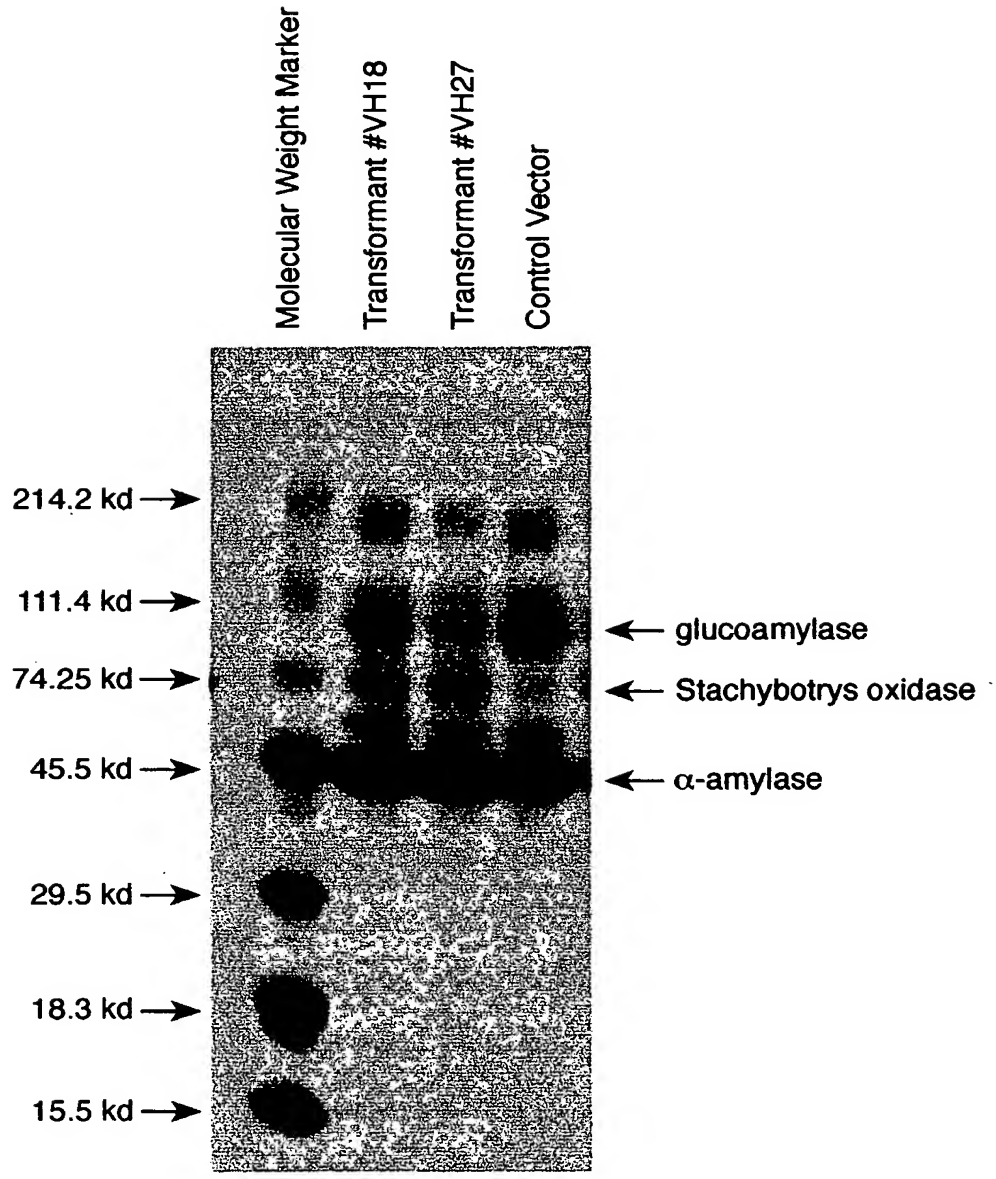
pGAPT Vector
5156 bps
glaA Terminator
2000
3000
glaA Terminator
A. nidulans pyrG

FIG._4

```
AGATCTAATA TGCTGTTCAA GTCATGGCAA CTGGCAGCAG CCTCCGGGCT CCTGTCTGGA  60
GTCCTCGGCA TCCCGATGGA CACCGGCAGC CACCCCATTG AGGCTGTTGA TCCCGAAGTG 120
AAGACTGAGG TCTTCGCTGA CTCCCTCCTT GCTGCAGCAG GCGATGACGA CTGGGAGTCA 180
CCTCCATACA ACTTGCTTTA CAGGTGAGAC ACCTGTCCCA CCTGTTTTCC CTCGATAACT 240
AACTCTTATA GGAATGCCCT GCCAATTCCA CCTGTCAAGC AGCCCAAGAT GTATGTCTTT 300
GATTTTCTAC GAAGCAACTC GGCCCCGACT AATGTATTCT AGGATCATTA CCAACCCTGT 360
CACCGGCAAG GACATTTGGT ACTATGAGAT CGAGATCAAG CCATTTCAGC AAAGGGTGAG 420
TTTGCTCAGA AACCTTGTGG TAATTAATCA TTGTTACTGA CCCTTTCAGA TTTACCCCAC 480
CTTGCGCCCT GCCACTCTCG TCGGCTACGA TGGCATGAGC CCTGGTCCTA CTTTCAATGT 540
TCCCAGAGGA ACAGAGACTG TAGTTAGGTT CATCAACAAT GCCACCGTGG AGAACTCGGT 600
CCATCTGCAC GGCTCCCCAT CGCGTGCCCC TTTCGATGGT TGGGCTGAAG ATGTGACCTT 660
CCCTGGCGAG TACAAGGATT ACTACTTTCC CAACTACCAA TCCGCCCGCC TTCTGTGGTA 720
CCATGACCAC GCTTTCATGA AGGTATGCTA CGAGCCTTTA TCTTTCTTGG CTACCTTTGG 780
CTAACCAACT TCCTTTCGTA GACTGCTGAG AATGCCTACT TTGGTCAGGC TGGCGCCTAC 840
ATTATCAACG ACGAGGCTGA GGATGCTCTC GGTCTTCCTA GTGGCTATGG CGAGTTCGAT 900
ATCCCTCTGA TCCTGACGGC CAAGTACTAT AACGCCGATG GTACCCTGCG TTCGACCGAG 960
GGTGAGGACC AGGACCTGTG GGGAGATGTC ATCCATGTCA ACGGACAGCC ATGGCCTTTC 1020
CTTAACGTCC AGCCCCGCAA GTACCGTTTC CGATTCCTCA ACGCTGCCGT GTCTCGTGCT 1080
TGGCTCCTCT ACCTCGTCAG GACCAGCTCT CCCAACGTCA GAATTCCTTT CCAAGTCATT 1140
GCCTCTGATG CTGGTCTCCT TCAAGCCCCC GTTCAGACCT CTAACCTCTA CCTTGCTGTT 1200
GCCGAGCGTT ACGAGATCAT TATTGGTATG CCCTCCCCTC TCACGAATGA GTCAAGAACT 1260
CTAAGACTAA CACTTGTAGA CTTCACCAAC TTTGCTGGCC AGACTCTTGA CCTGCGCAAC 1320
GTTGCTGAGA CCAACGATGT CGGCGACGAG GATGAGTACG CTCGCACTCT CGAGGTGATG 1380
CGCTTCGTCG TCAGCTCTGG CACTGTTGAG GACAACAGCC AGGTCCCCTC CACTCTCCGT 1440
GACGTTCCTT TCCCTCCTCA CAAGGAAGGC CCCGCCGACA AGCACTTCAA GTTTGAACGC 1500
AGCAACGGAC ACTACCTGAT CAACGATGTT GGCTTTGCCG ATGTCAATGA GCGTGTCCTG 1560
GCCAAGCCCG AGCTCGGCAC CGTTGAGGTC TGGGAGCTCG AGAACTCCTC TGGAGGCTGG 1620
AGCCACCCCG TCCACATTCA CCTTGTTGAC TTCAAGATCC TCAAGCGAAC TGGTGGTCGT 1680
GGCCAGGTCA TGCCCTACGA GTCTGCTGGT CTTAAGGATG TCGTCTGGTT GGGCAGGGGT 1740
GAGACCCTGA CCATCGAGGC CCACTACCAA CCCTGGACTG GAGCTTACAT GTGGCACTGT 1800
CACAACCTCA TTCACGAGGA TAACGACATG ATGGCTGTAT TCAACGTCAC CGCCATGGAG 1860
GAGAAGGGAT ATCTTCAGGA GGACTTCGAG GACCCCATGA ACCCCAAGTG GCGCGCCGTT 1920
CCTTACAACC GCAACGACTT CCATGCTCGC GCTGGAAACT TCTCCGCCGA GTCCATCACT 1980
GCCCGAGTGC AGGAGCTGGC CGAGCAGGAG CCGTACAACC GCCTCGATGA GATCCTGGAG 2040
GATCTTGGAA TCGAGGAGTA GTCTAGA                                      2067
```

FIG._5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Transformant #VH27
Control Vector
214.2 kd
111.4 kd
74.25 kd
45.5 kd
29.5 kd
18.3 kd
15.5 kd
glucoamylase
Stachybotrys oxidase
α-amylase

FIG._6